## Docket No.: PF-0221-3 DIV Inventors: Lal and Bandman

## Title: NOVEL HUMAN SODIUM-DEPENDENT PHOSPHATE COTRANSPORTER

Serial No.: To Be Assigned

5	' AG	A AC	9 G GT	G AG	G AT		C GA				G AG.		C TA	G GT.	45 A CG	c ca	T GC	54 C AGG
	TCA	CCG	63 GTC	CGG	CAA	72 TTC		GGT			ACG			CTT		GGG		108 CTG
	GGT	TCA	117 ACT	TGA	AGC	126 CCT	TCC	ACA		ATT		144 TCG		AAA	153 ACC	ATT	CAC	162 TAG
	GAG	AGG	171 AGA	AAC	ACA	180 ATG	GCC			ACA		198 TTG		ccc	207 ACA		AGG	216 GAG
	AGC <sup>,</sup>	AAG	225 AAC	GCA	CAA	234 GAT	ATG M	CAA Q	243 GTG V	GAT D	GAG E	252 ACA T	CTG L	ATC I	261 CCC P	AGG R	AAA K	270 GTT V
	CCA P		279 TTA L	TGT C	TCT S	288 GCT A	CGC R	TAT Y		ATA I			GTC V	TTA L	315 CAT H	TTC F	TGC C	324 AAT N
	TTC F		333 ACG T	ATA I	GCA A	342 CAA Q		GTC V		ATG M	AAC N	360 ATC I		ATG M	369 GTA V	GCC A	ATG M	378 GTC V
	AAC N	AGC S	387 ACA T	AGC S	CCT P	396 CAA Q	TCC S	CAG Q	405 CTC L	AAT N	GAT D	414 TCC S	TCT S	GAG E	423 GTG V	CTG L	CCT P	432 GTT V
		· TCA S		ggt G	GGC G		AGT S			CCA P		468 AGT S	CTT L	CCT P	477 GCA A		TCC S	486 TCA S
	ATA I	CTT L	495 GGG G	GGT G	CAG Q	504 TTT F	GCA A	ATT I	513 TGG W	gaa E	AGG R	522 TGG W	GGC G	CCT P.	531 CCA P	CAA Q	GAA E	540 CGA R
							GCT A		TCA			TTA		GGA		TTT		594 GCC A
		CTC L		GGT G			ATT			ACC			TGG		639 TTT F	GTC	TTC F	648 TAT Y
				GGT G			TGT			TGC			TGG			GTG		

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GAT D	GAC D	711 CCC P	GTT V	TCC S	720 TAT Y	CCA P	TGG W	729 ATA I	AGC S	ACC T	738 TCA S	GAA E	AAA K	747 GAA E	TAC Y	ATC I	756 ATA I
TCC S	TCC S	765 TTG L	AAA K	CAA Q	774 CAG Q	GTC V	GGG G	783 TCT S	TCT S	AAG K	792 CAG Q	CCT P	CTT L	801 CCC P	ATC I	AAA K	810 GCT A
ATG M	CTC L	819 AGA R	TCT S	CTA L	828 CCC P	ATT I	TGG W	837 TCC S		TGT C	846 TTA L		TGT C	855 TTC F	AGC S	CAT H	864 CAA Q
TGG W	TTA L	873 GTT V	AGC S	ACA T		GTT V	GTA V	891 TAC Y		CCA P	900 ACT T	TAC Y	ATC I	909 AGC S	TCT S	GTG V	918 TAC Y
CAT H	GTT V	927 AAC N	ATC I	AGA R	936 GAC D	AAT N	GGA G	945 CTT L	CTA L	TCT S	954 GCC A	CTT L	CCT P	963 TTT F	ATT I	GTT V	972 GCC A
TGG W	GTC V	981 ATA I	GGC G	ATG M	990 GTG V	GGA G	GGC G	999 TAT Y	CTG L		1008 GAT D	TTC F		1017 CTA L	ACC T		1026 AAG K
TTT F		1035 CTC L	ATC I		L044 GTG V	AGG R		1053 ATT I			1062 ATT I	TTA L		1071 AGT S	CTC L		1080 TCT S
TCA S	GCA		ATT I		1098 TCT S	CTG L	CCT	1107 TAC Y			1116 TCC S			1125 ATC I	ACA T		1134 ACT T
GCC A	TTG	1143 CTG L	ACG T		1152 TCT S	TGC C		1161 TTA L			1170 TTG L	TGT		1179 TCA S	GGG G		1188 TAT Y
ATC I		1197 GTC V	TTA L		1206 ATT I	GCT A		1215 AGG R	TAT Y		1224 AGT S	TTT F		1233 ATG M	GGA G		1242 TCA S
	GGA			AGC	ATA		CCT		ATT	GTA		ACT	GTC		GGA	TTT	1296 CTT L
	AGT	CAG	GAC	CCT	GAG	TTT	GGG	TGG	AGG	AAT		TTC	TTC	TTG	CTG	TTT	1350 GCC A
	AAC	CTG	TTA	GGA	CTA	CTC	TTC	TAC	CTC	ATA	1386 TTT F	GGA	GAA		GAT	GTC	1404 CAA Q

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Title: NOVEL HUMAN SODIUM-DEPENDENT PHOSPHATE COTRANSPORTER

Serial No.: To Be Assigned

\$1413\$ \$1422\$ \$1431\$ \$1440\$ \$1449\$ \$1458\$ GAA TGG GCT AAA GAG AGA AAA CTC ACT CGT TTA TGA AGT TAT CCC ACC TTG GAT E W A K E R K L T R L

1467 1476 1485 1494 1503 1512 GGA AAA GTC ATT AGG CAC CGT ATT GCA TAA AAT AGA AGG CTT CCG TGA TGA AAA

1521 1530 1539 1548 1557 1566 TAC CAG TGA AAA GAT TTT TTT TTC CTG TGG CTC TTT TCA ATT ATG AGA TCA GTT

1575 1584 1593 1602 1611 1620 CAT TAT TTT ATT CAG ACT TTT TTT TGA GAG AAA TGT AAG ATG AAT AAA AAT TCA

1629 1638 AAT AAA ATG ATA ACT AAG AAT GC 3'

### Docket No.: PF-0221-3 DIV Inventors: Lal and Bandman

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1 M Q V D B T L I P R K V 1 M Q M D N R L P P R K L A G R A L 16 C S A 16 C S A 17 C N V T M N T T M V M W N S T 18 C N L G V A I V S M V N N S 19 D P E T V G L I L S S T S Y G V 112 D P E T V G L I H G S F F W G Y 114 D P E T V G L I H G S F F W G Y 115 C L S S V L S L L I P P A A G I 150 V A T S T L N M L I P S A A R V 151 C L S S V L S L L I P P A A G I 152 V A T S T L N M L I P S A A R V 154 C I M S K M A P P L E R S R L A 155 E I L V V K M A P P L E R S R L A 156 E I L V V K M A P P L E R S R L A 157 C A T S T L S L L I P S A A R V 158 C I M S K M A P P L E R S R L A 159 C I M S K M A P P L E R S R L A 171 E Y I T S S L K Q Q V C 172 E Y I T S S L K Q Q V C 173 E Y I T S S L K Q Q V C 174 E Y I T S S L Y C Q V C 175 E Y I T S S L Y C Q V C 176 E Y I T S S L Y C Q V C 177 E Y I T S S L Y C Q V C 177 E Y I T S S L Y C Q V C 178 E Y I T S S L Y C Q V C 179 E Y I T S S L Y C Q V C 170 E Y I T S S L Y C Q V C 170 E Y I T S S L Y C Q V C 170 E Y I T S S L Y C Q V C 170 E Y I T S S L Y C Q V C 170 E Y I T S S L Y C Q V C 170 E Y I T S S L Y C Q V C 170 E Y I T S S L Y C Q V C 170 E Y I T S S L Y C Q V C 170 E Y I T S S L Y C Q V C 170 E Y I T S S L Y C Q V C 170 E Y I T S S L Y C Q V C 170 E Y I T S S L Y C Q V C 170 E Y I T S S L Y C Q V C 170 E Y I T S S L Y C Q V C 170 E Y I T S S L Y C Q V C 170 E Y I T S S L Y C Q V C 170 E Y I T S S L Y C Q V C 170 E Y C Y C C C C C C C C C C C C C C C C
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# Docket No.: PF-0221-3 DIV Inventors: Lal and Bandman

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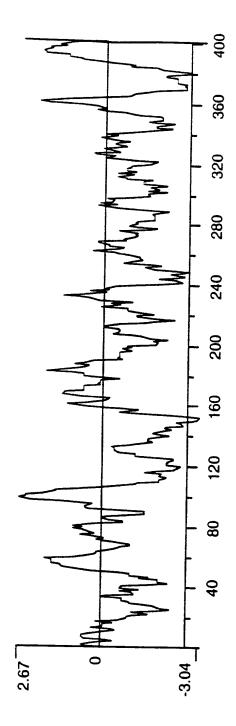
207 FSHOWLVSTMVVYIPTYISSVYHVNIRDNGLLSALPFIVA 272 FTFFWSHNIMTLYTPMFINSMLHVNIKENGFLSSLPYLFA 312 FCRSWTFYLLLISQPAYFEEVFGFEISKVGLVSALPHLVM	I R D N G L L S A L P F I V A 754412  I K E N G F L S S L P Y L F A G I 450532  I S K V G L V S A L P H L V M G I 507415
247 WVIGMVGGYLADFLLTKK-FRLITVRKIATILGSLPSSAL	RKIATILGSLPSSAL 754412
312 WICGNLAGQLSDFFLTRNILSVIAVRKLFTAAGFLLPAIF	RKLFTAAGFLLPAIF GI 450532
352 TIIVPIGGQIADFLRSRHIMSTTNVRKLMNCGGFGMEATL	RKLMNCGGFGMEATL GI 507415
286 IVSLPYLNSGYITATALLTLSCGLSTLCOSGIYINVLDIA	TLCOSGIYINVLDIA 754412
352 GWCLPYLSSTFYSIVIFLILAGATGSFGLGGVFLNGLDIA	SFICLGIGVFINGLDIA GI 450532
392 LLVVGYSHSKGVAIS-FLVLAVGFSGFAISGFNVNHLDIA	GFAI[SGFNV]NHLDIA GI 507415
326 PRYSSFLMGASRGFSSIAPVIVPTVSGFLLSQDPEFGWRN	SGFLLSQDPEFGWRN 754412
392 PRYFGFIKACSTLTGMIGGLIASTLTGLILKQDPESAWFK	TGLILKQDPESAWFK GI 450532
431 PRYASILMGISNGVGTLSGMVCPIIVGAMTKHKTREEWQY	VGAMTKHKTREEWQY GI 507415
366 <u>VFFLLFAVNLLGLLFYLIFGEADVQEWAKERKLTR</u>	EWAKERKLTR 754412
432 <u>TFILIMAAINVTGLIFYLIVATAEIQDWAKEKQHTR</u>	DWAKERQHIR GI 450532
471 <u>VF</u> LIASLUHYGGVIFYGVFASGEKOPWAEPEEMSE	PWAEPERSEKCGF GI 507415
401	
401 L	754412
467 L	GI 450532
551 PRPPPVRDY	GI 507415

# FIGURE 2E

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Title: NOVEL HUMAN SODIUM-DEPENDENT PHOSPHATE COTRANSPORTER

Serial No.: To Be Assigned

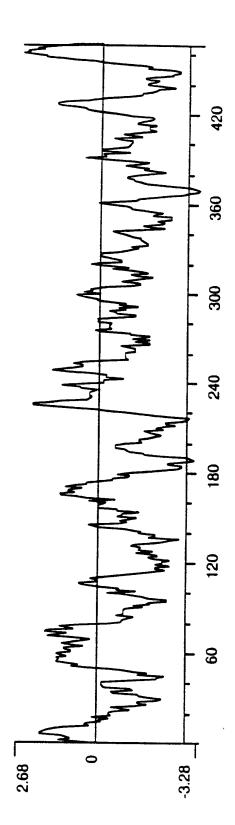


IGURE 3A

Inventors: Lal and Bandman

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